

RAW SEQUENCE LISTING

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Application Serial Number: 10/511,269
Source: PCF
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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/511,269

DATE: 04/14/2006
 TIME: 11:14:33

Input Set : F:\260276US0PCT.txt
 Output Set: N:\CRF4\04142006\J511269.raw

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3 <110> APPLICANT: MORI, HIROSHI
5 <120> TITLE OF INVENTION: GAMMA-SECRETASE INHIBITORS
7 <130> FILE REFERENCE: 260276US0PCT
9 <140> CURRENT APPLICATION NUMBER: 10/511,269
10 <141> CURRENT FILING DATE: 2004-10-20
12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/050117
13 <151> PRIOR FILING DATE: 2003-04-18
15 <150> PRIOR APPLICATION NUMBER: JP2002-121983
16 <151> PRIOR FILING DATE: 2002-04-24
18 <160> NUMBER OF SEQ ID NOS: 13
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 17
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
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30 1 5 10 15
33 Lys
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38 <211> LENGTH: 6
39 <212> TYPE: PRT
40 <213> ORGANISM: Homo sapiens
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49 <211> LENGTH: 4
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51 <213> ORGANISM: Homo sapiens
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55 Leu Val Met Leu
56 1
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 4
61 <212> TYPE: PRT
62 <213> ORGANISM: Homo sapiens
64 <400> SEQUENCE: 4
66 Thr Leu Val Met
67 1
70 <210> SEQ ID NO: 5
71 <211> LENGTH: 11
72 <212> TYPE: PRT

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73 <213> ORGANISM: Homo sapiens
 75 <400> SEQUENCE: 5
 77 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 78 1 5 10
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 82 <211> LENGTH: 2088
 83 <212> TYPE: DNA
 84 <213> ORGANISM: Homo sapiens
 87 <220> FEATURE:
 88 <221> NAME/KEY: CDS
 89 <222> LOCATION: (1)..(2088)
 91 <400> SEQUENCE: 6
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 93 Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
 94 1 5 10 15
 96 gcg ctg gag gta ccc act gat ggt aat gct ggc ctg ctg gct gaa ccc 96
 97 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
 98 20 25 30
 100 cag att gcc atg ttc tgt ggc aga ctg aac atg cac atg aat gtc cag 144
 101 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 102 35 40 45
 104 aat ggg aag tgg gat tca gat cca tca ggg acc aaa acc tgc att gat 192
 105 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 106 50 55 60
 108 acc aag gaa ggc atc ctg cag tat tgc caa gaa gtc tac cct gaa ctg 240
 109 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 110 65 70 75 80
 112 cag atc acc aat gtg gta gaa gcc aac caa cca gtg acc atc cag aac 288
 113 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 114 85 90 95
 116 tgg tgc aag cgg ggc cgc aag cag tgc aag acc cat ccc cac ttt gtg 336
 117 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 118 100 105 110
 120 att ccc tac cgc tgc tta gtt ggt gag ttt gta agt gat gcc ctt ctc 384
 121 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 122 115 120 125
 124 gtt cct gac aag tgc aaa ttc tta cac cag gag agg atg gat gtt tgc 432
 125 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 126 130 135 140
 128 gaa act cat ctt cac tgg cac acc gtc gcc aaa gag aca tgc agt gag 480
 129 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 130 145 150 155 160
 132 aag agt acc aac ttg cat gac tac ggc atg ttg ctg ccc tgc gga att 528
 133 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 134 165 170 175
 136 gac aag ttc cga ggg gta gag ttt gtg tgt tgc cca ctg gct gaa gaa 576
 137 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 138 180 185 190
 140 agt gac aat gtg gat tct gct gat gcg gag gag gat gac tcg gat gtc 624

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141	Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
142		195			200					205						
144	tgg	tgg	ggc	gca	gac	aca	gac	tat	gca	gat	ggg	agt	gaa	gac	aaa	672
145	Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
146		210			215				215		220					
148	gta	gta	gaa	gta	gca	gag	gag	gaa	gtg	gct	gag	gtg	gaa	gaa	gaa	720
149	Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	
150	225				230					235			240			
152	gaa	gcc	gat	gat	gac	gag	gac	gat	gag	gat	ggt	gat	gag	gta	gag	768
153	Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	
154		245			250				250		255					
156	gag	gct	gag	gaa	ccc	tac	gaa	gaa	gcc	aca	gag	aga	acc	acc	agc	att
157	Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
158		260			265				265		270					
160	gcc	acc	acc	acc	acc	acc	aca	gag	tct	gtg	gaa	gag	gtg	gtt	cga	864
161	Ala	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg						
162		275			280				280		285					
164	gtt	cct	aca	aca	gca	gcc	agt	acc	cct	gat	gcc	gtt	gac	aag	tat	ctc
165	Val	Pro	Thr	Thr	Ala	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu
166		290			295				295		300					
168	gag	aca	cct	ggg	gat	gag	aat	gaa	cat	gcc	cat	ttc	cag	aaa	gcc	aaa
169	Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys
170	305				310				310		315			320		
172	gag	agg	ctt	gag	gcc	aag	cac	cga	gag	aga	atg	tcc	cag	gtc	atg	aga
173	Glu	Arg	Leu	Glu	Ala	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg
174		325			330				330		335					
176	gaa	tgg	gaa	gag	gca	gaa	cgt	caa	gca	aag	aac	ttg	cct	aaa	gct	gat
177	Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp
178		340			345				345		350					
180	aag	aag	gca	gtt	atc	cag	cat	ttc	cag	gag	aaa	gtg	gaa	tct	ttg	gaa
181	Lys	Lys	Ala	Val	Ile	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu
182		355			360				360		365					
184	cag	gaa	gca	gcc	aac	gag	aga	cag	cag	ctg	gtg	gag	aca	cac	atg	gcc
185	Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala
186		370			375				375		380					
188	aga	gtg	gaa	gcc	atg	ctc	aat	gac	cgc	cgc	cgc	ctg	gcc	ctg	gag	aac
189	Arg	Val	Glu	Ala	Met	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn
190	385				390				390		395			400		
192	tac	atc	acc	gct	ctg	cag	gct	gtt	cct	cct	cgt	cac	gtg	ttc		1248
193	Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe
194		405			410				410		415					
196	aat	atg	cta	aag	aag	tat	gtc	cgc	gca	gaa	cag	aag	gac	aga	cag	cac
197	Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His
198		420			425				425		430					
200	acc	cta	aag	cat	ttc	gag	cat	gtg	cgc	atg	gtg	gat	ccc	aag	aaa	gcc
201	Thr	Leu	Lys	His	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala
202		435			440				440		445					
204	gct	cag	atc	cgg	tcc	cag	gtt	atg	aca	cac	ctc	cgt	gtg	att	tat	gag
205	Ala	Gln	Ile	Arg	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu

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206	450	455	460	
208	cgc atg aat cag tct ctc tcc ctg ctc tac aac gtc cct gca gtg gcc			1440
209	Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala			
210	465	470	475	480
212	gag gag att cag gat gaa gtt gat gag ctg ctt cag aaa gag caa aac			1488
213	Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn			
214	485	490	495	
216	tat tca gat gac gtc ttg gcc aac atg att agt gaa cca agg atc agt			1536
217	Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser			
218	500	505	510	
220	tac gga aac gat gct ctc atg cca tct ttg acc gaa acg aaa acc acc			1584
221	Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr			
222	515	520	525	
224	gtg gag ctc ctt ccc gtg aat gga gag ttc agc ctg gac gat ctc cag			1632
225	Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln			
226	530	535	540	
228	ccg tgg cat tct ttt ggg gct gac tct gtg cca gcc aac aca gaa aac			1680
229	Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn			
230	545	550	555	560
232	gaa gtt gag cct gtt gat gcc cgc cct gct gcc gac cga gga ctg acc			1728
233	Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr			
234	565	570	575	
236	act cga cca ggt tct ggg ttg aca aat atc aag acg gag gag atc tct			1776
237	Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser			
238	580	585	590	
240	gaa gtg aag atg gat gca gaa ttc cga cat gac tca gga tat gaa gtt			1824
241	Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val			
242	595	600	605	
244	cat cat caa aaa ttg gtg ttc ttt gca gaa gat gtg ggt tca aac aaa			1872
245	His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys			
246	610	615	620	
248	ggt gca atc att gga ctc atg gtg ggc ggt gtt gtc ata gcg aca gtg			1920
249	Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val			
250	625	630	635	640
252	atc gtc atc acc ttg gtg atg ctg aag aag aaa cag tac aca tcc att			1968
253	Ile Val Ile Thr Leu Val Met Leu Lys Lys Gln Tyr Thr Ser Ile			
254	645	650	655	
256	cat cat ggt gtg gtg gag gtc gac gcc gct gtc acc cca gag gag cgc			2016
257	His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg			
258	660	665	670	
260	cac ctg tcc aag atg cag cag aac ggc tac gaa aat cca acc tac aag			2064
261	His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys			
262	675	680	685	
264	tcc ttt gag cag atg cag aac tag			2088
265	Phe Phe Glu Gln Met Gln Asn			
266	690	695		
269	<210> SEQ ID NO: 7			
270	<211> LENGTH: 695			
271	<212> TYPE: PRT			

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272 <213> ORGANISM: Homo sapiens
 274 <400> SEQUENCE: 7
 276 Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
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 280 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
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 284 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 285 35 40 45
 288 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 289 50 55 60
 292 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 293 65 70 75 80
 296 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 297 85 90 95
 300 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 301 100 105 110
 304 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 305 115 120 125
 308 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 309 130 135 140
 312 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 313 145 150 155 160
 316 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 317 165 170 175
 320 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 321 180 185 190
 324 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 325 195 200 205
 328 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 329 210 215 220
 332 Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 333 225 230 235 240
 336 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 337 245 250 255
 340 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 341 260 265 270
 344 Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 345 275 280 285
 348 Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
 349 290 295 300
 352 Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
 353 305 310 315 320
 356 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
 357 325 330 335
 360 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
 361 340 345 350
 364 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
 365 355 360 365
 368 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala

VERIFICATION SUMMARY

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